

D. Srinivastava

1653

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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/808,031A**

DATE: 05/06/1999
TIME: 08:25:11

INPUT SET: S31745.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

#30

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori

10 (ii) TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE

(iii) NUMBER OF SEQUENCES: 52

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: WEISER & ASSOCIATES
16 (B) STREET: 230 South Fifteenth Street, Suite 500
17 (C) CITY: Philadelphia
18 (D) STATE: PA
19 (E) COUNTRY: USA
20 (F) ZIP: 19102

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

29 (A) APPLICATION NUMBER: US 08/808,031
30 (B) FILING DATE: 03-MAR-1997
31 (C) CLASSIFICATION:

32
33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Weiser, Gerard J.
35 (B) REGISTRATION NUMBER: 19,763
36 (C) REFERENCE/DOCKET NUMBER: 377(913).5888P

38 (ix) TELECOMMUNICATION INFORMATION:

39 (A) TELEPHONE: 215-875-8383
40 (B) TELEFAX: 215-875-8394

43 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2176 base pa

**RAW SEQUENCE LISTING
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47 (B) TYPE: nucleic acid
 48 (C) STRANDEDNESS: double
 49 (D) TOPOLOGY: linear
 50
 51 (ii) MOLECULE TYPE: cDNA
 52
 53
 54 (ix) FEATURE:
 55 (A) NAME/KEY: CDS
 56 (B) LOCATION: 640..2094
 57
 58
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 60
 61 TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG 60
 62 TGTACCGCGT TTCCCTGGAT GGTACACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT 120
 63 CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG 180
 64 CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCCTCGGCA TTGGTCTAAA 240
 65 CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG 300
 66 ACGACGTGCG CTTCACGCCG GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC 360
 67 CTCGAGCGGC GGAGCGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG 420
 68 TAGCCTGTTT TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGTA GCGGAGCCAA 480
 69 CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG 540
 70 CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT 600
 71 GTCCCGTCTT CCATGCCCGC GCCCAGCCAA GGTGCAGAC ATG ACC GCC AGG CTG 654
 72 Met Thr Ala Arg Leu
 73 1 5
 74
 75 GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG 702
 76 Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu
 77 10 15 20
 78
 79 CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG 750
 80 Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg Glu Ala Arg Arg
 81 25 30 35
 82
 83
 84 CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG 798
 85 Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala
 86 40 45 50
 87
 88 GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC 846
 89 Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu
 90 55 60 65

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100	GGC GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG	894
101	Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys	
102	70 75 80 85	
103		
104	GCC TGG AAG GAG AAG AAG GCG GAG GCC ACC GAG CGC CGC GCG CTG	942
105	Ala Trp Lys Glu Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu	
106	90 95 100	
107		
108	AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG	990
109	Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu	
110	105 110 115	
111		
112	GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC	1038
113	Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp	
114	120 125 130	
115		
116	GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG	1086
117	Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu	
118	135 140 145	
119		
120	GAC TCC GCG GAG GCG CTG GCC AAG GCG CTG GGG CTG AGC GTC TCC AAG	1134
121	Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly Leu Ser Val Ser Lys	
122	150 155 160 165	
123		
124	CTC CGC TGG TTC GCG TTC CAC CGG GAG GTC GAC ACG GCC ACG CAC TAC	1182
125	Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr	
126	170 175 180	
127		
128	GTG AGC TGG ACC ATT CCG AAG CGG GAC GGC AGC AAG CGC ACG ATT ACG	1230
129	Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr	
130	185 190 195	
131		
132	TCC CCC AAG CCT GAG CTG AAG GCA GCG CAG CGC TGG GTG CTG TCC AAC	1278
133	Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn	
134	200 205 210	
135		
136	GTC GTG GAG CGG CTG CCG GTC CAC GGC GCC GCC CAC GGC TTC GTG GCG	1326
137	Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala	
138	215 220 225	
139		
140	GGA CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTC	1374
141	Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val	
142	230 235 240 245	
143		
144	GTG GTC AAG GTG GAC CTC AAG GAC TTC TTC CCC TCC GTC ACC TGG CGC	1422
145	Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg	
146	250 255 260	
147		
148	CGG GTG AAG GGC CTG TTG CGC AAG GGC GGC CTG CGG GAG GGC ACG TCC	1470
149	Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser	
150	265 270 275	
151		
152		

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153	ACG CTG CTG TCC CTC CTC TCC ACG GAA GCG CCG CGG GAG GCG GTC CAG	1518
154	Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln	
155	280	285
156		
157	TTC CGC GGC AAG CTC CTG CAC GTC GCC AAG GGC CCG CGC GCC CTG CCC	1566
158	Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro	
159	295	300
160		
161	CAG GGC GCC CCC ACG TCG CCC GGC ATC ACC AAC GCG CTC TGC CTG AAG	1614
162	Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys	
163	310	315
164		
165	CTC GAC AAG CGG CTG TCC GCC CTC GCG AAG CGG CTG GGC TTC ACC TAC	1662
166	Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr	
167	330	335
168		
169	ACG CGC TAC GCG GAC GAC CTG ACC TTC TCC TGG ACG AAG GCG AAG CAG	1710
170	Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln	
171	345	350
172		
173	CCC AAG CCG CGG CGG ACG CAG CGT CCC CCC GTC GCG GTC CTC CTG TCT	1758
174	Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser	
175	360	365
176		
177	CGC GTC CAG GAA GTG GTG GAG GCG GAG GGC TTC CGC GTG CAC CCG GAC	1806
178	Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp	
179	375	380
180		
181	AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC	1854
182	Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu	
183	390	395
184		
185	GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC	1902
186	Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg	
187	410	415
188		
189	GAC GTC GTC CGC CAG CTC CGC GCC ATC CAC AAC CGG AAG AAG GGC	1950
190	Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly	
191	425	430
192		
193	AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC	1998
194	Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala	
195	440	445
196		
197	GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT	2046
198	Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala	
199	455	460
200		
201	CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG	2094
202	Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu	
203	470	475
204		
205	TGACGGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCCGCC AGCAACGCCG CATTCAAGCAA	2154

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206
207 CTCCGTCAGC CGGCAGCGGGT AC 2176
208
209
210 (2) INFORMATION FOR SEQ ID NO:2:
211
212 (i) SEQUENCE CHARACTERISTICS:
213 (A) LENGTH: 485 amino acids
214 (B) TYPE: amino acid
215 (D) TOPOLOGY: linear
216
217 (ii) MOLECULE TYPE: protein
218
219 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
220
221 Met Thr Ala Arg Leu Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala
222 1 5 10 15
223
224 Val Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys
225 20 25 30
226
227 Arg Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys
228 35 40 45
229
230 Ala Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu
231 50 55 60
232
233 Val Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser
234 65 70 75 80
235
236 Glu Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr
237 85 90 95
238
239 Glu Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr
240 100 105 110
241
242 His Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
243 115 120 125
244
245 Ala Asp Ala Phe Asp Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn
246 130 135 140
247
248 Gly Leu Thr Glu Leu Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly
249 145 150 155 160
250
251 Leu Ser Val Ser Lys Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp
252 165 170 175
253
254 Thr Ala Thr His Tyr Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser
255 180 185 190
256
257 Lys Arg Thr Ile Thr Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg
258 195 200 205

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SEQUENCE VERIFICATION REPORT
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Original Text